Rapid mRNA decay mechanisms: Insight from genetic and genomic approaches

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Highly unstable mRNAs are of particular interest in eukaryotes because they allow organisms to respond rapidly to internal and external stimuli. One pathway for rapid mRNA decay in Arabidopsis is mediated by an mRNA instability sequence called DST that is highly conserved in the 3' untranslated regions of unstable Small-Auxin-Up-RNAs (*SAUR*s). A genetic selection for mutants with defects in the pathway led to the isolation of *dst1*, *dst2* and *dst3*. These mutants elevate the level of two transgene mRNAs, *HPH-DST* and *GUS-DST,* and an endogenous DST-containing mRNA called *SAUR-AC1*. To understand more about the molecular phenotypes of *dst1*, we compared gene expression in the mutant with that of the parental line using DNA microarrays of 11,000 Arabidopsis ESTs. These studies identified new genes with altered mRNA abundance in the mutants, a number of which contain DST-like elements and are presumably primary targets of the *dst1* defect. About a third of the transcripts that change in *dst1* are circadian regulated. This is higher than would be expected by chance and may indicate an association of the DST-mediated decay pathway and the circadian clock. Interestingly, we also observed a circadian association in another study aimed at identifying the most inherently unstable mRNAs represented on the 11K microarrays. By hybridizing the arrays with probes corresponding to RNA before and after transcription was inhibited for two hours, we found that at least 1% of the transcripts represented decayed with half-lives of less than 60 minutes. These unstable transcripts encode proteins that are predicted to participate in a broad range of cellular processes, with transcriptional functions being over-represented relative to the whole Arabidopsis genome annotation. Analysis of public microarray expression data for these genes argues that mRNA instability is of high significance during plant responses to mechanical stimulation and is associated with specific genes controlled by the circadian clock. Supported by NSF, USDA and DOE.